

SEQUENCE PROTOCOL

<110> Degussa AG

<120> Nucleotide sequences which code for the ppvK gene

<130> 000569 BT

<140>

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1239

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (237) ..(1022)

<223> ppvK gene

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cgcttatccc tgatacgtac agcggtaagc gtggcagttt ccgcggcgat ggcacgcaac 180
tcattaaacg attgttgttc cataagacca tcacgttgtt ttttttagaa aattgc ctg 239
Met
1
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cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga 287
Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly
5 10 15
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ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac 335
Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn
20 25 30
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ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct 383
Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro
35 40 45
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aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att 431
Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile
50 55 60 65
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tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tgg gtc 479
Ser Gln Ala Glu Thr Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val
70 75 80
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gtt cgc ggg cag atc cgc cta tcc gca gcc aac att gac aag tcc tgg 527
Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp
85 90 95
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atc ggc acc gat gtg cac gaa ctt ttt gac cgc cac cta aat ggc cga 575
Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg
100 105 110

gag atc acc gtt ctc aat gac gca gac gcc gcc ggc atc gcc gaa gca 623
Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu Ala
115 120 125

acc ttt ggc aac cct gcc gca cgc gaa ggc gca gtc atc ctg ctg acc 671
Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu Thr
130 135 140 145

ctt ggt aca ggt att gga tcc gca ttc ctt gtg gat ggc caa ctg ttc 719
Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu Phe
150 155 160

ccc aac aca gaa ctc ggt cac atg atc gtt gac ggc gag gaa gca gaa 767
Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala Glu
165 170 175

cac ctt gca gca gca tcc gtc aaa gaa aac gaa gat ctg tca tgg aag 815
His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp Lys
180 185 190

aaa tgg gcg aag cac ctg aac aag gtg ctg agc gaa tac gag aaa ctt 863
Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys Leu
195 200 205

ttc tcc cca tcc gtc ttc atc atc ggt ggc gga att tcc aga aag cac 911
Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Ile Ser Arg Lys His
210 215 220 225

gaa aag tgg ctt cca ttg atg gag cta gac act gac att gtc cca gct 959
Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro Ala
230 235 240

gag ctg cgc aat cga gcc gga atc gta gga gct gcc atg gca gta aac 1007
Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val Asn
245 250 255

caa cac ctc acc cca taagttatcg aaaggtgatt ttgcccagg gccttgattc 1062
Gln His Leu Thr Pro
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acaacgcacc ttgctgtagg aaaaacaggc ccctttgtga catcggcgta gttgttcaac 1122

tataatggaa cgctgatcgt ggacaagagt taaccatgag attgattcac ccctttaagc 1182

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 35 40 45
 Pro Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile
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 Ile Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser
 65 70 75 80
 Val Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser
 85 90 95
 Trp Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly
 100 105 110
 Arg Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu
 115 120 125
 Ala Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu
 130 135 140
 Thr Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu
 145 150 155 160
 Phe Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala
 165 170 175
 Glu His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp
 180 185 190
 Lys Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys
 195 200 205
 Leu Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys
 210 215 220
 His Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro
 225 230 235 240
 Ala Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val
 245 250 255
 Asn Gln His Leu Thr Pro
 260